

## WHAT IS CLAIMED IS:

1. An isolated nucleic acid molecule, wherein said nucleic acid molecule encodes at least a portion of a plant retroelement reverse transcriptase and comprises a nucleic acid sequence selected from the group consisting of:
- (a) a nucleic acid sequence having more than 85% identity to a nucleic acid sequence selected from the group consisting of even-numbered SEQ ID NOs inclusive from SEQ ID NO 42 to SEQ ID NO 164, wherein said identity can be determined using the DNAsis computer program and default parameters;
  - (b) a nucleic acid sequence which encodes an amino acid sequence having more than 85% identity to an amino acid sequence selected from the group consisting of odd-numbered SEQ ID NOs inclusive from SEQ ID NO 43 through SEQ ID NO 165, wherein said identity can be determined using the DNAsis computer program and default parameters;
  - (c) a nucleic acid sequence which encodes an allelic variant of a nucleic acid sequence selected from the group consisting of: a nucleic acid sequence of (a); a nucleic acid sequence of (b).
  - (d) a nucleic acid sequence fully complementary to a nucleic acid sequence selected from the group consisting of: a nucleic acid sequence of (a); a nucleic acid sequence of (b).
2. A seed comprising a nucleic acid of claim 1.
3. A plant comprising a nucleic acid of claim 1.

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4. A nucleic acid molecule of 1, which comprises gag, pol and env genes and which comprises adenine-thymidine-guanidine as the gag gene start codon.
5. A nucleic acid molecule of claim 2, which further comprises SEQ ID NO 5.
6. An isolated nucleic acid molecule of claim 1, wherein said nucleic acid molecule encodes at least a portion of a plant envelope sequence and comprises a nucleic acid sequence selected from the group consisting of:
  - (a) a nucleic acid sequence which has more than 90% identity to SEQ ID NO 5, wherein said identity can be determined using the DNAsis computer program and default parameters;
  - (b) a nucleic acid sequence which encodes an amino acid sequence which has greater than 85% identity to SEQ ID NO 6, wherein said identity can be determined using the DNAsis computer program and default parameters;
  - (c) a nucleic acid sequence which encodes an allelic variant of SEQ ID NO 5; and
  - (d) a nucleic acid sequence fully complementary to a nucleic acid sequence selected from the group consisting of: a nucleic acid sequence of (a); a nucleic acid sequence of (b); and a nucleic acid sequence of c).
7. A plant cell comprising an isolated nucleic acid molecule of claim 6.
8. A method to impart agronomically-significant characteristics to at least one plant cell, comprising:

contacting a nucleic acid molecule of claim 6 to at least one plant cell under conditions sufficient to allow at least one agronomically-significant nucleic acid molecule to enter said cell.

9. An isolated nucleic acid molecule, wherein said nucleic acid molecule encodes at least a portion of a plant retroelement reverse transcriptase and comprises a nucleic acid sequence selected from the group consisting of:

(a) a nucleic acid sequence having more than 95% identity to a nucleic acid sequence selected from the group consisting of even-numbered SEQ ID NOs inclusive from SEQ ID NO 42 to SEQ ID NO 164, wherein said identity can be determined using the DNAsis computer program and default parameters;

(b) a nucleic acid sequence which encodes an amino acid sequence having more than 95% identity to an amino acid sequence selected from the group consisting of odd-numbered SEQ ID NOs inclusive from SEQ ID NO 43 through SEQ ID NO 165, wherein said identity can be determined using the DNAsis computer program and default parameters;

(c) a nucleic acid sequence which encodes an allelic variant of a nucleic acid sequence selected from the group consisting of: a nucleic acid sequence of (a); a nucleic acid sequence of (b).

(d) a nucleic acid sequence fully complementary to a nucleic acid sequence selected from the group consisting of: a nucleic acid sequence of (a); a nucleic acid sequence of (b).

10. A seed comprising a nucleic acid of claim 9.

11. A plant comprising a nucleic acid of claim 9.
12. A nucleic acid molecule of 9, which comprises gag, pol and env genes and which comprises adenine-thymidine-guanidine as the gag gene start codon.
13. A nucleic acid molecule of claim 9, which further comprises SEQ ID NO 5.
14. A method to impart agronomically-significant characteristics to at least one plant cell, comprising:

contacting a nucleic acid molecule of claim 9 to at least one plant cell under conditions sufficient to allow at least one agronomically-significant nucleic acid molecule to enter said cell.

15. An isolated nucleic acid molecule, wherein said nucleic acid molecule encodes at least a portion of a plant retroelement reverse transcriptase and comprises a nucleic acid sequence selected from the group consisting of:

(a) a nucleic acid sequence selected from the group consisting of even-numbered SEQ ID NOs inclusive from SEQ ID NO 42 to SEQ ID NO 164, wherein said identity can be determined using the DNAsis computer program and default parameters;

(b) a nucleic acid sequence which encodes an amino acid sequence selected from the group consisting of odd-numbered SEQ ID NOs inclusive from SEQ ID NO 43 through SEQ ID NO 165, wherein said identity can be determined using the DNAsis computer program and default parameters;

(c) a nucleic acid sequence which encodes an allelic variant of a nucleic acid sequence selected from the group consisting of: a nucleic acid sequence of (a); a nucleic acid sequence of (b).

(d) a nucleic acid sequence fully complementary to a nucleic acid sequence selected from the group consisting of: a nucleic acid sequence of (a); a nucleic acid sequence of (b).

16. A seed comprising a nucleic acid of claim 15.

17. A plant comprising a nucleic acid of claim 15.

18. A nucleic acid molecule of 15, which comprises gag, pol and env genes and which comprises adenine-thymidine-guanidine as the gag gene start codon.

19. A nucleic acid molecule of claim 9, which further comprises SEQ ID NO 5.

20. A method to impart agronomically-significant characteristics to at least one plant cell, comprising:

contacting a nucleic acid molecule of claim 15 to at least one plant cell under conditions sufficient to allow at least one agronomically-significant nucleic acid molecule to enter said cell.

21. A nucleic acid molecule of claim 15, which further comprises at least one nucleic acid sequence which encodes at least one agronomically-significant characteristic.

22. A nucleic acid molecule of claim 21, wherein the agronomically-significant characteristic is selected from the group consisting of: male sterility; self-incompatibility; foreign organism resistance;

improved biosynthetic pathways; environmental tolerance; photosynthetic pathways; and nutrient content.

23. A nucleic acid molecule of claim 21, wherein the agronomically significant characteristic is selected from the group consisting of: fruit ripening; oil biosynthesis; pigment biosynthesis; seed formation; starch metabolism; salt tolerance; cold/frost tolerance; drought tolerance; tolerance to anaerobic conditions; protein content; carbohydrate content (including sugars and starches); amino acid content; and fatty acid content.

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24. An isolated plant retroviral particle comprising a nucleic acid molecule of claim 15.

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25. A plant of claim 17, which plant is selected from the group consisting of: soybean; maize; sugar cane; beet; tobacco; wheat; barley; poppy; rape; sunflower; alfalfa; sorghum; rose; carnation; gerbera; carrot; tomato; lettuce; chicory; pepper; melon; cabbage; oat; rye; cotton; flax; potato; pine; walnut; citrus (including oranges, grapefruit etc.); hemp; oak; rice; petunia; orchids; Arabidopsis; broccoli; cauliflower; brussel sprouts; onion; garlic; leek; squash; pumpkin; celery; pea; bean (including various legumes); strawberries; grapes; apples; pears; peaches; banana; palm; cocoa; cucumber; pineapple; apricot; plum; sugar beet; lawn grasses; maple; triticale; safflower; peanut; and olive.

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